MYCOTAXON

ISSN (print) 0093-4666 (online) 2154-8889 © 2016. Mycotaxon, Ltd.

October–December 2016—Volume 131, pp. 859–869

http://dx.doi.org/10.5248/131.859

Discopycnothyrium palmae gen. & sp. nov. (*Asterinaceae*)

Sinang Hongsanan[1,2], Ali H. Bahkali[3], Putarak Chomnunti[*1,2], Jian-Kui Liu[1,2], Jun-Bo Yang[4] & Kevin D. Hyde[1,2,3]

[1] *Institute of Excellence in Fungal Research, Mae Fah Luang University, Chiang Rai, 57100, Thailand*

[2] *School of Science, Mae Fah Luang University, Chiang Rai, 57100, Thailand*

[3] *Department of Botany and Microbiology, College of Sciences, King Saud University, Riyadh, KSA*

[4] *Germplasm Bank of Wild Species in Southwest China, Kunming Institute of Botany, Chinese Academy of Science, Kunming 650201, Yunnan, China*

* Correspondence to: *putarak.cho@mfu.ac.th*

Abstract—A new genus and species, *Discopycnothyrium palmae*, is described from palms (*Arecaceae*) in Narathiwat Province, southern Thailand, and is known only from its asexual morph. The genus is characterized by circular pycnothyria with darkened cells around the central ostiole, variably long hyphae at the margin, and pycnothyriospores that are 1-septate with the septum between a larger brown upper cell and hyaline lower cell. LSU gene sequence analysis clustered *D. palmae* in the *Asterinaceae* clade and supported (59% ML and 0.88 PP support) the taxon as phylogenetically distinct from other *Asterinaceae*. Morphological and phylogenetic differences confirm the new genus, here introduced and illustrated.

Key words—*Asterinales*, foliar epiphytes, taxonomy

Introduction

The family *Asterinaceae* was introduced by Hansford (1946), with the generic type *Asterina* Lév. (Müller & von Arx 1962, Luttrell 1973, Eriksson 1981, Hosagoudar 2004, Kirk et al. 2008, Hofmann 2010, Hyde et al. 2013, Hongsanan et al. 2014). The family comprises biotrophs found on living plant leaves and is distributed worldwide (Kirk et al. 2001, Barr & Huhndorf 2001, Taylor et al., Hofmann et al. 2010, Hyde et al. 2013, Hongsanan et al. 2014). While most previous studies focused on the morphology, Hofmann (2010) provided the first molecular data of *Asterinaceae* that supported its phylogenetic

placement in *Dothideomycetes* and which were included in the phylogenetic tree representing *Asterinales* sensu stricto (Hyde et al. 2013, 2016, Wijayawardene et al. 2014). The order comprises a single family *Asterinaceae,* which contains 17 genera that are differentiated using both morphological and phylogenetic characters (Hongsanan et al. 2014). The asexual morph in the family can be either coelomycetous (*Asterostomella*) or hyphomycetous (*Asterina*), although classification of the asexual morphs needs further clarification (Hyde et al. 2013, Hongsanan et al. 2014). Redescription of the asexual morphs of *Asterinaceae* (Hofmann 2010, Hosagoudar 2010) and key to genera by Hosagoudar (2010) were based mainly on morphology and host association

In this study, we introduce a new genus *Discopycnothyrium* and its type species *D. palmae* based on phylogeny, morphology, and host association. *Discopycnothyrium* is an asexual morph genus that somewhat resembles *Asterostomula* and *Prillieuxina* in its circular pycnothyria with radially arranged cells. However, *Asterostomula* and *Prillieuxina* differ in having pycnothyria with star-like or irregular openings and brown pycnothyriospores, while pycnothyria in *Discopycnothyrium* have a central ostiole and 1-septate pycnothyriospores comprising brown upper cells and hyaline lower cells. The placement of *Discopycnothyrium* in *Asterinaceae* is also supported by rDNA sequence analysis.

Materials & methods

An *Asterinaceae*-like specimen was collected from Narathiwat Province in the southern part of Thailand. Morphological characters were observed under Nikon 80i stereo and compound microscopes. Measurements were determined using Tarosoft (R) Image Frame Work (v. 0.9.7). We attempted to isolate the specimen by using a single spore technique (Chomnunti et al. 2011, 2014), but the spores did not grow in culture. The fresh specimen was therefore dried in silica gel, and DNA was extracted directly from pycnothyria. Type material was conserved in the Herbarium, Center of Excellence in Fungal Research, Mae Fah Luang University, Chiang Rai, Thailand (MFLU), and the Herbarium, Kunming Institute of Botany, Chinese Academy of Sciences, Kunming, China (KUN).

Genomic DNA was extracted from dried pycnothyria using the E.Z.N.A® Forensic Genomic DNA Extraction Kit (OMEGA Bio-tek Norcross GA 2013). Individual pycnothyria were placed into 1.5 ml sterilized tubes and kept in -20 °C overnight, after which DNA was extracted following the manufacturer's instructions.

Universal primers LR5 and LROR were successfully used to amplify the 28S rDNA (LSU) region. The PCR thermal cycle program was: an initial cycle at 94°C for 3 min; 40 cycles of denaturation (94°C for 30 s), annealing (54°C for 40 s), elongation (72°C for 1 min); final extension (72°C for 10 min). After visualization on 1% agarose electrophoresis gels stained with ethidium bromide, the PCR products were sent to

Table 1. Taxa used in the phylogenetic analysis: specimen codes and GenBank accession numbers (LSU)

Species	Voucher/culture	GenBank no.
Apiosporina collinsii	CBS 118973	GU301798
Asterina cestricola	TH 591	GU586215
Asterina fuchsiae	TH 590	GU586216
Asterina phenacis	TH589	GU586217
Asterina siphocampyli	ppMP 1324	HQ701140
Asterina sp.	MFLU13-0619	KM386978
Asterina weinmanniae	TH 592	GU586218
Asterina zanthoxyli	TH 561	GU586219
Discopycnothyrium palmae	**MFU13-0485**	**KM386979**
Asterotexis cucurbitacearum	PMA M-0141224	HQ610510
Chaetothyriothecium elegans	CPC 21375	KF268420
Coleroa robertiani	CBS 458.64	JQ036231
Fusicladium africanum	CPC 12828	EU035423
Fusicladium pini	CBS 463.82	EU035436
Gibbera conferta	CBS 191.53	GU301814
Gloniopsis praelonga	CBS 112415	FJ161173
Gloniopsis subrugosa	CBS:123346	FJ161210
Hysterium angustatum	CBS 236.34	FJ161180
Hysterobrevium smilacis	CBS 114601	FJ161174
Lembosia albersii	MFLU13-0377	KM386982
Lichenothelia convexa	L1608	KC015085
Microthyrium microscopicum	CBS 115976	GU301846
Natipusilla limonensis	L_AF286_1A	HM196370
	PE3_2b	JX474862
Natipusilla naponensis	L_AF217_1A	HM196371
Oedohysterium insidens	CBS:238.34	FJ161142
Oedohysterium sinense	CBS:123345	FJ161209
Protoventuria barriae	CBS 300.93	JQ036232
Psiloglonium araucanum	CBS:112412	FJ161172
Psiloglonium clavisporum	CBS:123338	FJ161197
Psiloglonium simulans	CBS:206.34	FJ161178
Rhytidhysteron rufulum	AFTOL-ID 2109	FJ469672
Sympoventuria capensis	CPC 12840	DQ885904
	CBS 120136	KF156104
Tyrannosorus pinicola	AFTOL-ID 1235	DQ470974
Venturia inaequalis	CBS 815.69	GU301878
Veronaeopsis simplex	CBS 588.66	EU041877
Zeloasperisporium siamense	IFRDCC 2194	JQ036228

*LSU: 28s rDNA (Newly generated sequence in bold)

Majorbio Co., Ltd. (China) for purification and sequencing. The sequence generated for *Discopycnothyrium palmae* was deposited in GenBank (KM386979).

Other LSU sequence data in this study were obtained from GenBank to compile the dataset (Table 1), which represents *Asterinaceae*, *Hysteriaceae* Chevall., *Microthyriaceae* Sacc., *Mytilinidiaceae* Kirschst., *Natipusillaceae* Raja et al., *Sympoventuriaceae* Y. Zhang ter et al., and *Venturiaceae* E. Müll. & Arx ex M.E. Barr following the publications by Schoch et al. (2009), Hyde et al. (2013), Boonmee et al. (2014), Hongsanan et al. (2014), and Wijayawardene et al. (2014). *Lichenothelia convexa* Henssen was selected as outgroup. Alignments were performed automatically using BioEdit v 7.1.9 and Clustal X 2.0.11 (Thompson et al. 1997) and improved manually when necessary (Hall 2004).

Maximum likelihood analysis was performed in RAxML with raxmlGUIv.0.9b2 (Silvestro & Michalak 2012); the search strategy was set to rapid bootstrapping and carried out using GTRGAMMAI model of nucleotide substitution for a small dataset to account for rate heterogeneity. The nucleotide substitution model was selected with MrModel test 2.2 (Nylander 2008); the number of replicates was automatically inferred using the stopping criterion (Pattengale et al. 2009). The evolution model was performed with MrModeltest 2.2 (Nylander 2008). Posterior probabilities (PP) (Rannala & Yang 1996, Zhaxybayeva & Gogarten 2002) were determined by Markov Chain Monte Carlo sampling (MCMC) in MrBayes (v. 3.0b4; Huelsenbeck & Ronquist 2001). Six simultaneous Markov chains ran for 1,000,000 generations, with trees sampled every 100th generation. 10,000 trees were obtained; the first 2000 trees, representing the burn-in phase were discarded, and the remaining 8000 trees were used to calculate posterior probabilities; the default convergence criterion was set at 0.001 (Cai et al. 2006, 2008). Phylogenetic trees were viewed in TreeView (v. 1.6.6; Page 2001). Maximum likelihood bootstrap values higher than 50% are given as the first set of numbers above the nodes (Fig. 2). Bayesian posterior probabilities (BYPP) equal or higher than 0.9 are given as the second set of numbers above the nodes (Fig. 2).

Taxonomy

Discopycnothyrium Hongsanan & K.D. Hyde, **gen. nov.**

Index Fungorum IF551024

Differs from other genera in *Asterinaceae* by its pycnothyria with darker cells surrounding a rounded central ostiole, and 1-septate pycnothyriospores with a hyaline lower cell.

Type Species: *Discopycnothyrium palmae* Hongsanan & K.D. Hyde

Etymology: from Latin *disco* meaning "circular" or "plate-like", and *pycnothyrium* referring to the technical term for the type of fructification.

Faces of Fungi FoF00569

Foliar epiphytes. Superficial mycelium aseptate, pale brown to brown. Sexual morph: undetermined. Asexual morph: pycnothyrium superficial on the host surface, circular, walls comprising radially arranged cells, dark brown, with central ostiole surrounded by dark cells. Peridium poorly

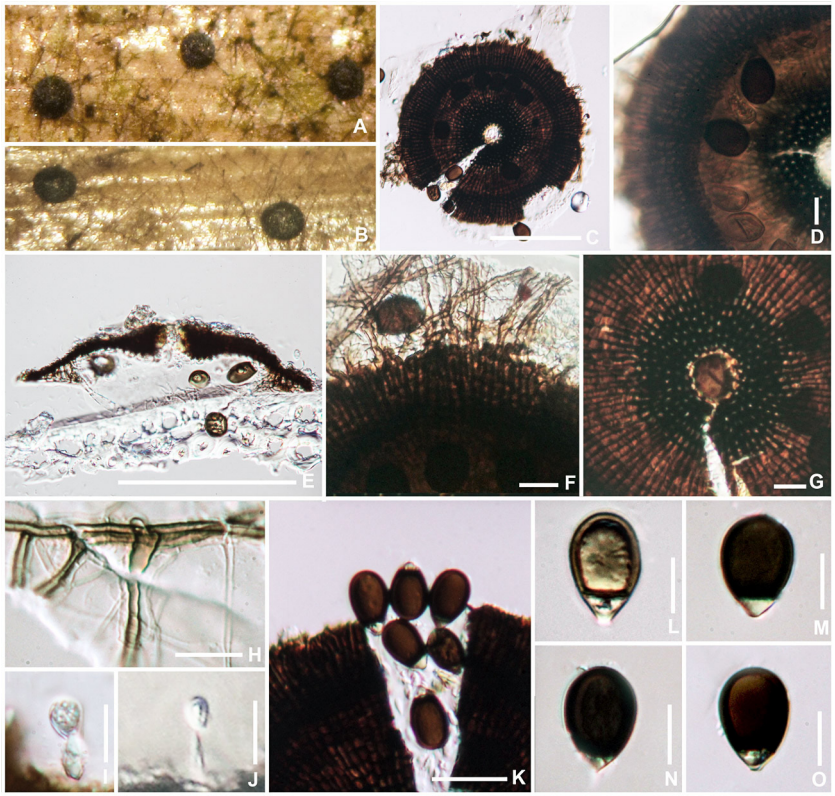

Fig 1. *Discopycnothyrium palmae* (MFLU 13-0485, holotype). A, B. Pycnothyria on surface of host. C. Pycnothyrium when viewed in squash mounts. D. Pycnothyriospore arrangement in pycnothyrium. E. Vertical section through pycnothyrium. F. Upper wall of pycnothyrium when viewed in squash mounts. G. Darkened cells around ostiole. H. Aseptate hyphae without appressoria. I, J. Conidiogenous cells giving rise to pycnothyriospores. K, M–O. Mature pycnothyriospore. L. Immature pycnothyriospore. Bars: C–E = 100 µm; K = 20 µm; D, F–J, L–O = 10 µm.

developed at the base. Conidiogenous cells holoblastic, cylindrical, hyaline. Pycnothyriospores ovoid or broadly clavate, widest and rounded near the apex and tapering towards lower end, 1-septate near the tapering base, upper cell pale brown to brown, lower cell hyaline.

Discopycnothyrium palmae Hongsanan & K.D. Hyde, **sp. nov.** Fig. 1

Index Fungorum IF551023

Differs from other species in *Asterinaceae* by its darker brown cells surrounding a rounded central ostiole, and its 1-septate pycnothyriospores with a hyaline lower cell.

Type: Thailand, Narathiwat Province, on the branches of palm (*Arecaceae*), September 2013, K.D. Hyde (**holotype** MFLU13-0485; **isotype** KUN; GenBank KM386979).

Etymology: Referring to the host palm on which the fungus was found.

Faces of Fungi FoF00570

Foliar epiphytes on surface of palm leaves (*Arecaceae*). Superficial mycelium 1–2 µm diam (x = 2 µm, n = 10), aseptate, pale brown to brown, dark brown at the margin, lacking appressoria and setae.

Sexual morph: Undetermined.

Asexual morph: Pycnothyrium 162–195 µm diam (x = 187 µm, n = 10), superficial on host surface, easily removed, mostly solitary, circular, hyphae of different lengths at the margin, wall comprising radial cells, dark brown, with central ostiole, and with darker cells around the central ostiole. Peridium poorly developed at the base. Pseudoparaphyses not observed. Conidiophores not observed. Conidiogenous cells 6–8 × 2–3 µm (x = 8 × 3 µm, n = 5), holoblastic in cavity of pycnothyria, cylindrical, hyaline, smooth. Pycnothyriospores 18–22 × 12–15 µm (x = 20 × 13 µm, n = 10), ovoid or broadly clavate, widest and rounded near the apex and tapering towards the lower end, 1-septate near the tapering base, not constricted at the septum, upper cell with 2 layers when immature, outer layer disappearing at maturity, pale brown in upper cell when immature and dark brown at maturity with smooth-walls, lower cell always hyaline, smooth-walled or sometimes rough.

Notes: *Discopycnothyrium palmae* is most similar to *Asterostomula loranthi* Theiss. by having a superficial mycelium without appressoria and setae and pycnothyrium walls composed of radial cells, but *A. loranthi* differs in the stellate dehiscence of the pycnothyrium centers and its unicellular pycnothyriospores (Hosagoudar 2010).

The new species also somewhat resembles the asexual morph of *Prillieuxina,* which also has circular pycnothyria and dark pycnothyriospores with a single septum, and a similar host association (Hofmann 2010), with *P. calami* (Syd. & P. Syd.) R.W. Ryan and *P. saginata* (Syd. & P. Syd.) R.W. Ryan also described from arecaceous hosts. *Prillieuxina* differs from *Discopycnothyrium* by its circular pycnothyria with X- or Y-shaped fissures at maturity and its 1-septate pycnothyriospores with a brown (not hyaline) lower cell (Hongsanan et al. 2014).

Allothyrium marcgraviae Syd. also has circular pycnothyria but differs from *D. palmae* by the star-like fissures of its pycnothyrial opening and its multi-septate ascospores (Hongsanan et al. 2014). The LSU sequence analyses cluster *D. palmae* in the clade of *Asterinaceae* but in its own lineage, with 59% ML and 0.88 PP support (Fig. 2), confirming it as a new genus.

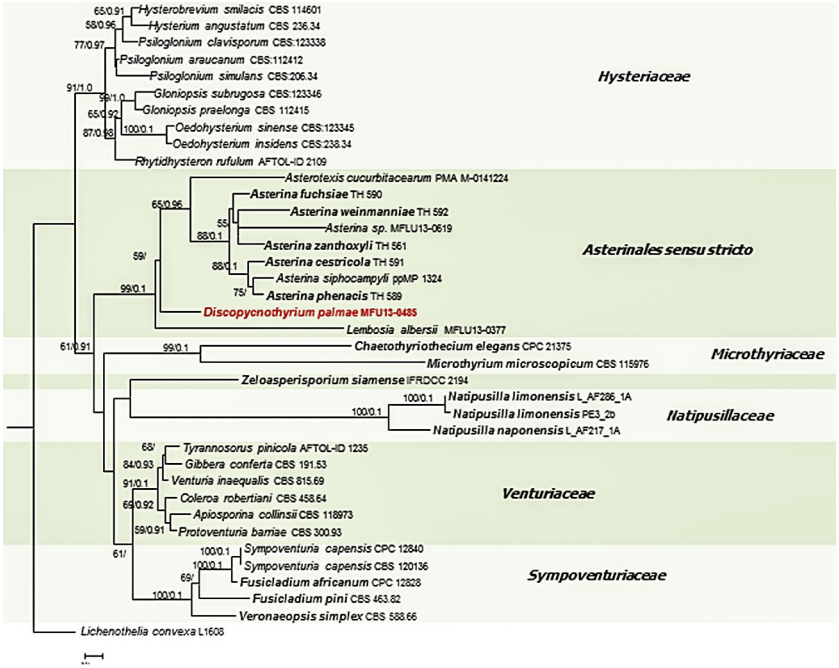

Fig 2. RAxML maximum likelihood phylogenetic tree based on sequence analysis of LSU dataset. The first set of numbers above the nodes are RAxML values >50%; the second set are Bayesian posterior probabilities ≥0.9. Strain numbers are indicated after species names. The new species introduced is in red bold, other types are in black bold.

Molecular phylogeny

LSU sequence data from six families (*Hysteriaceae*, *Microthyriaceae*, *Mytilinidiaceae*, *Natipusillaceae*, *Sympoventuriaceae*, *Venturiaceae*) were included in the phylogenetic analysis (Fig. 2). The *Asterinaceae* clade includes six strains of *Asterina*: *A. cestricola* (R.W. Ryan) Hosag. & T.K. Abraham, *A. fuchsiae* Syd., *A. phenacis* Syd., *A. siphocampyli* Syd., *A. weinmanniae* Syd., and *A. zanthoxyli* W. Yamam. The new taxon, *Discopycnothyrium palmae*, forms a moderately supported (59% ML, 0.88 PP) clade sister to the other *Asterina* species, supporting *D. palmae* as clearly separate from other species in *Asterinaceae*. Moreover, *Lembosia albersii* Henn. (MFLU13-0377) forms a well-supported clade basal to the other genera in *Asterinaceae* with high (99% ML, 1.0 PP) bootstrap support.

The *Microthyriaceae* clade comprises two strains: *Chaetothyriothecium elegans* Hongsanan & K.D. Hyde and *Microthyrium microscopicum* Desm.,

also with high (99% ML, 1.0 PP) bootstrap support. The *Natipusillaceae* clade includes three strains of freshwater fungi: *Natipusilla limonensis* A. Ferrer et al. (two strains) and *N. naponensis* A. Ferrer et al. with 100% ML and 1.0 PP support; although they are phylogenetically related to *Zeloasperisporium siamense* Hongsanan et al., there is no morphological similarity between *Natipusilla* and *Zeloasperisporium,* so these should be regarded as tentatively placed lineages.

The *Venturiaceae* clade) with high bootstrap support of 91% ML, 1.0 PP) includes six representative strains—*Apiosporina collinsii*(Schwein.) Höhn., *Coleroa robertiani* (Fr.) E. Müll., *Gibbera conferta* (Fr.) Petr., *Protoventuria barriae* Carris & A.P. Poole, *Tyrannosorus pinicola* (Petrini & P.J. Fisher) Unter. & Malloch, and *Venturia inaequalis* (Cooke) G. Winter.The clade of *Venturiaceae*—and is closely (66% ML support) related to the *Sympoventuriaceae* clade with five strains: *Sympoventuria capensis* Crous & Seifert (two strains), *Fusicladium africanum* Crous, *F. pini* Crous & de Hoog, and *Veronaeopsis simplex*(Papendorf) Arzanlou & Crous.

Discussion

Discopycnothyrium (type species *D. palmae*) is introduced as a new genus in the family *Asterinaceae* (characterised by a superficial pycnothyrium comprising radiating cells) that differs from other genera in having circular pycnothyria with variably long marginal hyphae, darkened cells around a central ostiole, and pycnothyriospores that are widest near the apex, taper towards lower end, and have one septum near the tapering base that separates the larger pale brown to brown upper cell from the smaller hyaline basal cell.

There are limited sequence data for taxa in *Asterinaceae* because members of this family are mostly obligate parasites/biotrophs, and pure cultures are difficult to obtain; therefore direct DNA extraction and sequencing must be obtained from specimen. However, sequence data from *Asterina* species do support the *Asterinaceae* within *Dothideomycetes* (Hofmann 2010, Wu et al. 2011, Hyde et al. 2013, Boonmee et al. 2014, Hongsanan et al. 2014, Wijayawardene et al. 2014). Although phylogenetic LSU analyses of *Discopycnothyrium* cluster *D. palmae* within the *Asterinaceae* clade, it is distinctly separate from other genera in that clade. Bootstrap values are not high because of low number of populations representing this group, and further study is needed to clarify the divergence of the species. Based on

Nonetheless, both morphology and phylogeny supports the new taxon as a species in a new genus within *Asterinaceae*, which we introduce here as *Discopycnothyrium*.

Acknowledgments

The authors extend their sincere appreciations to the Deanship of Scientific Research at King Saud University for its funding this Prolific Research group (PRG-1436-9). We thank the reviewers Hiran Ariyawansa (Guizhou Academy of Agricultural Sciences, Guizhou University) and Ying Zhang (Institute of Microbiology, Beijing Forestry University) for improving this manuscript.

Literature cited

Barr ME, Huhndorf SM. 2001. *Loculoascomycetes*. 283–305, in: DJ McLaughlin et al. (eds). The Mycota: Systematics and Evolution, Part A, vol. VII. Springer, Berlin. http://dx.doi.org/10.1007/978-3-662-10376-0_13

Boonmee S, Rossman AY, Liu JK, Li WJ, Dai DQ, Bhat JD, Jones EBG, McKenzie EHC, Xu JC, Hyde KD. 2014. *Tubeufiales*, ord. nov., integrating sexual and asexual generic names. Fungal Divers. 68: 239–298. http://dx.doi.org/10.1007/s13225-014-0304-7

Cai L, Jeewon R, Hyde KD. 2006. Phylogenetic investigations of *Sordariaceae* based on multiple gene sequences and morphology. Mycol. Res. 110: 137–150. http://dx.doi.org/10.1016/j.mycres.2005.09.014

Cai L, Guo XY, Hyde KD. 2008. Morphological and molecular characterisation of a new anamorphic genus *Cheirosporium* from freshwater in China. Persoonia 20: 53–58. http://dx.doi.org/10.3767/003158508X314732

Chomnunti P, Schoch CL, Aguirre–Hudson B, KoKo TW, Hongsanan S, Jones EBG, Kodsueb R, Chukeatirote E, Bahkali AH, Hyde KD. 2011. *Capnodiaceae*. Fungal Divers. 51: 103–134. http://dx.doi.org/10.1007/s13225-011-0145-6

Chomnunti P, Hongsanan S, Aguirre-Hudson B, Tian Q, Peršoh D, Dhami MK, Alias AS, Xu J, Liu X, Stadler M, Hyde KD. 2014. The sooty moulds. Fungal Divers. 66: 1–36. http://dx.doi.org/10.1007/s13225-014-0278-5

Eriksson O. 1981. The families of bitunicate ascomycetes. Nord. J. Bot. 1(6): 800–800. http://dx.doi.org/10.1111/j.1756-1051.1981.tb01167.x

Hall TA. 2004. BioEdit. Ibis Therapeutics, Carlsbad, CA, 92008, USA [http://www.mbio.ncsu.edu/BioEdit/bioedit.html (18 March 2005)]

Hansford CG. 1946. The foliicolous ascomycetes, their parasites and associated fungi. Mycol. Papers 15: 1–240.

Hofmann TA. 2010. Plant parasitic *Asterinaceae* and *Microthyriaceae* from the Neotropics (Panama). PhD thesis. The faculty of biological sciences at the J.W. Goethe-University Frankfurt am Main, Germany. 408 p.

Hongsanan S, Li YM, Liu JK, Hofmann T, Piepenbring M, Bhat JD, Boonmee S, Doilom M, Singtripop C, Tian Q, Mapook A, Zeng XY, Bahkali AH, Xu JC, Wu XH, Yang JB, Hyde KD. 2014. Revision of genera in *Asterinales*. Fungal Divers. 68: 1–68. http://dx.doi.org/10.1007/s13225-014-0307-4

Hosagoudar VB. 2010. Anamorphs of *Asterinales*. J. Theor. Biol. 6(3 and 4): 199–211.

Hosagoudar VB, Biju CK, Abraham TK. 2004. Studies on foliicolous fungi. J. Econ. Taxon. Bot. 28: 175–182.

Huelsenbeck JP, Ronquist F. 2001. MRBAYES: Bayesian inference of phylogenetic trees. Bioinformatics 17(8): 754–755. http://dx.doi.org/10.1093/bioinformatics/17.8.754

Hyde KD, Jones EBG, Liu JK, Ariyawansa H, Boehm E, Boonmee S, Braun U, Chomnunti P, Crous PW, Dai DQ, Diederich P, Dissanayake A, Doilom M, Doveri F, Hongsanan S, Jayawardena R, Lawrey JD, Li YM, Liu YX, Lücking R, Monkai J, Muggia L, Nelsen MP, Pang KL, Phookamsak

R, Senanayake I, Shearer CA, Suetrong S, Tanaka K, Thambugala KM, Wijayawardene NN, Wikee S, Wu HX, Zhang Y, Aguirre-Hudson B, Alias SA, Aptroot A, Bahkali AH, Bezerra JL, Bhat DJ, Camporesi E, Chukeatirote E, Gueidan C, Hawksworth DL, Hirayama K, Hoog SD, Kang JC, Knudsen K, Li WJ, Li XH, Liu ZY, Mapook A, McKenzie EHC, Miller AN, Mortimer PE, Phillips AJL, Raja HA, Scheuer C, Schumm F, Taylor JE, Tian Q, Tibpromma S, Wanasinghe DN, Wang Y, Xu JC, Yan JY, Yacharoen S, Zhang M. 2013. Families of *Dothideomycetes*. Fungal Divers. 63: 1–313. http://dx.doi.org/10.1007/s13225-013-0263-4

Hyde KD, Hongsanan S, Jeewon R, Bhat DJ, McKenzie EHC, Jones EBG, Phookamsak R, Ariyawansa HA, Boonmee S, Zhao Q, Abdel-Aziz FA, Abdel-Wahab MA, Banmai S, Chomnunti P, Cui BK, Daranagama DA, Das K, Dayarathne MC, de Silva NL, Dissanayake AJ, Doilom M, Ekanayaka AH, Gibertoni TB, Góes-Neto A, Huang SK, Jayasiri SC, Jayawardena RS, Konta S, Lee HB, Li WJ, Lin CG, Liu JK, Lu YZ, Luo ZL, Manawasinghe IS, Manimohan P, Mapook A, Niskanen T, Norphanphoun C, Papizadeh M, Perera RH, Phukhamsakda C, Richter C, de Santiago ALCMA, Drechsler-Santos ER, Senanayake IC, Tanaka K, Tennakoon TMDS, Thambugala KM, Tian Q, Tibpromma S, Thongbai B, Vizzini A, Wanasinghe DN, Wijayawardene NN, Wu H, Yang J, Zeng XY, Zhang H, Zhang JF, Bulgakov TS, Camporesi E, Bahkali AH, Amoozegar AM, Araujo-Neta LS, Ammirati JF, Baghela A, Bhatt RP, Bojantchev S, Buyck B, da Silva GA, de Lima CLF, de Oliveira RJV, de Souza CAF, Dai YC, Dima B, Duong TT, Ercole E, Mafalda-Freire F, Ghosh A, Hashimoto A, Kamolhan S, Kang JC, Karunarathna SC, Kirk PM, Kytövuori I, Lantieri A, Liimatainen K, Liu ZY, Liu XZ, Lücking R, Medardi G, Mortimer PE, Nguyen TTT, Promputtha I, Raj KNA, Reck MA, Lumyong S, Shahzadeh-Fazeli SA, Stadler M, Soudi MR, Su HY, Takahashi T, Tangthirasunun N, Uniyal P, Wang Y, Wen TC, Xu JC, Zhang ZK, Zhao YC, Zhou JZ, Zhu L. 2016. Fungal diversity notes 367–491: taxonomic and phylogenetic contributions to fungal taxa. Fungal Divers. 81: 1–270.

Kirk PM, Cannon PF, David JC, Stalpers JA. 2001. Ainsworth & Bisby's dictionary of the fungi, 9th edn. CABI, Wallingford.

Kirk PM, Cannon PF, Minter DW, Stalpers JA. 2008. Ainsworth & Bisby's dictionary of the fungi, 10th edn. CABI, Wallingford.

Luttrell ES. 1973. *Loculoascomycetes*. 135–219, in: GC Ainsworth et al. (eds). The fungi: an advanced treatise. Academic Press.

Müller E, von Arx JA. 1962. Die Gattungen der didymosporen Pyrenomycten. Beitr. Kryptogamenfl. Schweiz 11(2). 992 p.

Nylander JAA, Wilgenbusch JC, Warren DL, Swofford DL. 2008. AWTY (are we there yet?): a system for graphical exploration of MCMC convergence in Bayesian phylogenetics. Bioinformatics 24: 581–583. http://dx.doi.org/10.1093/bioinformatics/btm388

Omega Bio-tek. 2013. E. Z. N. A. Forensic DNA Kit. www.omegabiotek.com

Page RDM. 2001. TreeView: Tree drawing software for Apple Macintosh and Windows. Available at http://taxonomy.zoology.gla.ac.uk/rod/treeview.html.

Pattengale ND, Alipour M, Bininda-Emonds ORP, Moret BME, Stamatakis A. 2009. How many bootstrap replicates are necessary?. LNCS 5541: 184–200. http://dx.doi.org/10.1089/cmb.2009.0179

Rannala B, Yang Z. 1996. Probability distribution of molecular evolutionary trees: a new method of phylogenetic inference. J. Mol. Evol. 43: 304–311. http://dx.doi.org/10.1007/BF02338839

Schoch CL, Crous PW, Groenewald JZ, Boehm EWA, Burgess TI, de Gruyter J, de Hoog GS, Dixon LJ, Grube M, Gueidan C, Harada Y, Hatakeyama S, Hirayama K, Hosoya T, Huhndorf SM, Hyde KD, Jones EBG, Kohlmeyer J, Kruys A, Li YM, Lücking R, Lumbsch HT, Marvanová L, Mbatchou JS, McVay AH, Miller AN, Mugambi GK, Muggia L, Nelsen MP, Nelson P, Owensby CA, Phillips AJL, Phongpaichit S, Pointing SB, Pujade-Renaud V, Raja HA, Rivas Plata E,

Robbertse B, Ruibal C, Sakayaroj J, Sano T, Selbmann L, Shearer CA, Shirouzu T, Slippers B, Suetrong S, Tanaka K, Volkmann-Kohlmeyer B, Wingfield MJ, Wood AR, Woudenberg JHC, Yonezawa H, Zhang Y, Spatafora JW. 2009. A class–wide phylogenetic assessment of *Dothideomycetes*. Stud. Mycol. 64: 1–15. http://dx.doi.org/10.3114/sim.2009.64.01

Silvestro D, Michalak I. 2012. RaxmlGUI: a graphical front-end for RAxML. Org. Divers. Evol. 12: 335–337. http://dx.doi.org/10.1007/s13127-011-0056-0

Taylor A, ST Hardy GE, Wood P, Burgess T, 2005. Identification and pathogenicity of *Botryosphaeria* species associated with grapevine decline in Western Australia. Australas. Plant Pathol. 34: 187–195. http://dx.doi.org/10.1071/AP05018

Thompson JD, Gibson TJ, Plewniak F, Jeanmougin F, Higgins DG. 1997. The CLUSTAL X windows interface: flexible strategies for multiple sequence alignment aided by quality analysis tools. Nucleic Acids Res. 25: 4876–4882. http://dx.doi.org/10.1093/nar/25.24.4876

Wijayawardene NN, Crous PW, Kirk PM, Hawksworth DL, Boonmee S, Braun U, Dai DQ, D'souza MJ, Diederich P, Dissanayake A, Doilom M, Hongsanan S, Jones EBG, Groenewald JZ, Jayawardena R, Lawrey JD, Liu JK, Lücking R, Madrid H, Manamgoda DS, Muggia L, Nelsen MP, Phookamsak R, Suetrong S, Tanaka K, Thambugala KM, Wikee S, Zhang Y, Aptroot A, Ariyawansa HA, Bahkali AH, Bhat DJ, Gueidan C, Chomnunti P, De Hoog GS, Knudsen K, McKenzie EHC, Miller AN, Phillips AJL, Piątek M, Raja HA, Shivas RS, Slippers B, Taylor JE, Tian Q. Wang Y, Woudenberg JHC, Cai L, Jaklitsch WM, Hyde KD. 2014. Naming and outline of *Dothideomycetes*–2014. Fungal Divers. 69: 1–55. http://dx.doi.org/10.1007/s13225-014-0309-2

Wu HX, Schoch CL, Boonmee S, Bahkali AH, Chomnunti P, Hyde KD. 2011. A reappraisal of *Microthyriaceae*. Fungal Divers. 51(1): 189–248. http://dx.doi.org/10.1007/s13225-011-0143-8

Zhaxybayeva O, Gogarten JP. 2002. Bootstrap, Bayesian probability and maximum likelihood mapping: exploring new tools for comparative genome analyses. BMC Genomics 3: 4. http://dx.doi.org/10.1186/1471-2164-3-4